

135 ITHQEMIKGI-----KKCTGGYRYDDMLVPIIENTPBEKGLKDRMAHANEYP 185
136 IANIQKAIKPSGVDPVTKPMALSF--DTLKPIIENMAHEDELIDDLHKTFRDYP 182
186 DSCAVLRRHGVYVNGETWEKAKTWCBCYDYLFDIAVSMKKVGLDPSOLPUGE 238
183 DTCVAVRRHGIFVNGPTIDKAKIFNEAIDYLMELAIKMYQMG1-PPDCGIGE 234

RESULT 2
T27523
hypothetical protein ZC373.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27523
R:Kershaw, J.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z20382
A:Accession: T27523
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-284 <WIL>
A:Cross-references: UNIPROT:Q23261; EMBL:Z49131; PIDN:CAA88977.1; GSPDB:GN000028; CESP:ZC373
A:Experimental source: clone ZC373
C:Genetics:
A:Gene: CBSP:ZC373.5
A:Map position: X
A:Introns: 26/3; 75/2; 114/1; 236/2

Query Match 32.6%; Score 431.5; DB 2; Length 284;
Best Local Similarity 39.9%; Pred. No. 2.6e-31;
Matches 87; Conservative 34; Mismatches 76; Indels 21; Gaps 1;

30 ELCKQFYHLGVTGTGGISLKHGDEIYIAPSGVQKRIQPEDMFVCDINEKDISGPS 89
35 ELMIQFYKLGWRGSGGAMGICSGSELMISPSALOKERIREQDVFFVNNKDKTEVQRPN 94
90 KLLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMTLLPPGREFKITHQEMIKGIKCTS 149
95 KRITVSSCVLFSLIIMKETSECVIHTHSKCANLITQLIKSNVFEISHQEIYKGIYDPS 154
150 GGYRYDDMLVPIIENTPBEKGL-----KDRMAHANEYPDSC 188
155 GKALKYSDTLTIPIIDNWPSESQLLVCAINRSPMQPDCFNIALFOEPIRGVLENYPOAI 214
189 AVLVRHGVYVNGETWEKAKTWCBCYDYLFDIAVSMKK 226
215 AVLVRNHGLFVWGPTWESTKIMTECIDYLLLELSIEMLK 252

RESULT 3
T39191
conserved hypothetical protein SPAC9.06c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39191
R:Wedler, H.; Duesterhoeft, A.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21834
A:Accession: T39191
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-192 <WED>
A:Cross-references: UNIPROT:Q9UT22; EMBL:AL121764; PIDN:CAB57424.1; GSPDB:GN000066; SPDB:
A:Experimental source: strain 972h-; cosmid c9
C:Genetics:
A:Gene: SPDB:SPAC9.06c
A:Map position: 1
A:Introns: 27/2; 53/2; 73/2; 129/1

Query Match 20.8%; Score 274.5; DB 2; Length 192;
Best Local Similarity 37.3%; Pred. No. 2.4e-17;

Matches 75; Conservative 29; Mismatches 76; Indels 21; Gaps 6;
QY 27 LIPELCKQFYHLGVT-CTGGISLKHGDEIYIAPSGVQKRIQPEDMFVCDINEKDISG 85
DB 9 LLELIPIPHYSLGMWKGSGYALCV-----KDRVQDRFTTENDIVTFNLN 54
QY 86 PSPSKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMTLLPPGREFKITHQEMIKGIK 145
DB 55 QSVTKDL--VWAYIFSWLNSMDAVACIYSTVAAGASMY--NEKFTTOSKEMIKGIP 110
QY 146 KCT-SGGYRYDDMLVPIIENTPBEKGLKDRMAHANEYPDSCAVLRRHGVYVNGETW 204
DB 111 KGNPSAGYLCCFTTLEVPPIHN-GDSKTLDELKKVIELYPOTCAVLIRGHGVIGWGATW 169
QY 205 EKAKTWCBCYDYLFDIAVSMKK 225
DB 170 EKSKTQMECYEYLFELDYLK 190

RESULT 4
A69864
conserved hypothetical protein ykry - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69864
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
leach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69860; MUID:98044033; PMID:9384377
A:Accession: A69864
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-209 <KUN>
A:Cross-references: UNIPROT:O31668; GB:Z99111; GB:AL009126; NID:g2636399; PIDN:CAB13234
A:Experimental source: strain 168
C:Genetics:
A:Gene: ykry
C:Superfamily: L-ribulose-phosphate 4-epimerase

Query Match 16.3%; Score 215.5; DB 2; Length 209;
Best Local Similarity 32.4%; Pred. No. 5.6e-12;
Matches 66; Conservative 32; Mismatches 87; Indels 19; Gaps 7;

QY 28 IPELCKQFYHLGVTGTGGISLKHGDEIYIAPSGVQKRIQPEDMFVCDIN-EKDI 83
DB 11 LAEVKRELAERDWPDPATSGNLISIKVTDEPLTFLVTASGDKRKETVEDFLVDQNGEPAE 70
QY 84 SQSPSKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMTLLPPGREFKITH--QEMI 141
DB 71 SGHS-----LKPSAETLLHLYNTNACCLHVVNNVISELY-GDQKLTFGQBI 125
QY 142 KGKKCTSGYRYDDMLVPIIENTPBEKGLKDRMAHANEYPDSCAVLRRHGVYVNG 201
DB 126 KAL-----GLWEENAEVTPPIENPAHPTLALFAEISE--DSGAVLIRNHGITAWG 177
QY 202 ETWEKAKTWCBCYDYLFDIAVSMKK 225
DB 178 KTAFAEKRVLEAYEFLFSYHLK 201

RESULT 5

H70469

L-fuculose-phosphate aldolase homolog - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: H70469
R/Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V

Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: H70469
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-208 <AQF>
A/Cross-references: UNIPROT:O67788; GB:AE000766; GB:AE000657; NID:g2984216; PIDN:AAC0775
A/Experimental source: strain VF5
C/Genetics:
A/Gene: fucA2
C/Superfamily: L-ribulose-phosphate 4-epimerase

Query Match 14.6%; Score 192.5; DB 1; Length 208;
Best Local Similarity 25.1%; Pred. No. 6.6e-10;
Matches 53; Conservative 37; Mismatches 94; Indels 27; Gaps 5;

QY 30 ELCKQP-----YHLGWVTGGGSLKHGDE-IYIAPSGVQKERIQPEDMF 74
DB 4 ELFKFSEKVEEIEAGRIILHSRGWVPATSGNISAKVSEYIAITASGKHGKLTPELIL 63
QY 75 VCDINEKDISGPSKSLKKSQCTPLPMNAYTM-RGAGAVIHTHSAANVATLLFQREF 133
DB 64 LIDYGRPVGGGKPSAE-----TLHTTVYKLPFVNAVVHTHSPNATVISIVEKKDFV 117
QY 134 KITHQEMIKGIKKCTSGYYRYDDMLVVPPIENTPEEKGLKDRMAHAMNEYPDSCAVLVR 193
DB 118 ELEDYELLKAFP-----DIHTHEVKIKIPFPNEQNIPLLAKEVENYKTSDEKYGFLIR 172
QY 194 RHGVYVNGETWEKAKTWCECYDYLFDIAVSM 224
DB 173 GHGLYTWGRSMEBALIHTALEPTEFCECLK 203

RESULT 6
D83436
probable sugar aldolase PA1683 [imported] - Pseudomonas aeruginosa (strain PAO1)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: D83436
R/Scover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bada
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: D83436
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-205 <STO>
A/Cross-references: UNIPROT:Q91342; GB:AE004595; GB:AE004091; NID:g9947644; PIDN:AAG0507
A/Experimental source: strain PAO1
C/Genetics:
A/Gene: PA1683

Query Match 12.6%; Score 166; DB 2; Length 205;
Best Local Similarity 26.3%; Pred. No. 1.6e-07;
Matches 49; Conservative 29; Mismatches 96; Indels 12; Gaps 4;

QY 36 YHLGWVTGGGSLKHGDE-IYIAPSGVQKERIQPEDMFVCDINEKDISGPSKSLKX 94
DB 20 YGRGWSPATSSNYSLRDLQALLTVSGKHGQLGFDVLA-----TDLAGNSLEPKKP 74
QY 95 SQCTPLPMNAYTWGA-GAVIHTHSAANVATLLFQREFPKITHQEMIKGIKKCTSGYY 153
DB 75 SAETLHTQLYAWNPAIGAVLHTHSAANVATLLVSLRVGRDLRVLDQVELQKAF-----AGVT 129

[illegible]

A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2209

Query Match	10.9%;	Score 144;	DB 2;	Length 218;
Best Local Similarity	23.7%;	Pred. No. 1.7e-05;		
Matches	49;	Conservative 32;	Mismatches 92;	Indels 34; Gaps 8;

Qy	34	QFYHLGVMTGTGGISLKHGD-EYIYAPSGVQKERIQPEDMFVCDINEKIDTSGP-SPEKK	91
Db	29	EFAAGWTPATSSNFSHRLDEHVAITVSGRDKCLTEEDIMAVDLGNVCHPTPSAE	88
Qy	92	LKKSQCTPLFNWAY-TWRGAGAVIHTHSKAAVMATLLFPGR-EPKITHQEMIKGIKKCTS	149
Db	89	-----TLHTQLYRRFPETGCVLHTSLTQTVAASRVYAGAGHISLKDYEELKAFE----	138
Qy	150	GGYRYDDMLVVPPIENTPBEKGL-----KDRMAHANNEYPDSCAVILVRHGGVTW	200
Db	139	-GHSTHETTLDPVPFCNTQNMNLLAAQVDLLDKQRM-----WGYLINGHGYTW	187
Qy	201	GETWEKAKTWCECYDYLFDAIVSMKKV	227
Db	188	GNTLADARRHLEALEFLHGLNELNLKL	214

RESULT 12
 A95238
 hypothetical protein SP2033 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: A95238
 R:Rettlein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:1357209; PMID:11463916
 A:Accession: A95238
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-227 <KUR>
 A:Cross-references: UNIPROT:Q9TNJ4; GB:AE005672; PIDN:AAK76098.1; PID:gl4973543; GSPDB:G
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP2033
 C:Superfamily: L-ribulose-phosphate 4-epimerase

Query Match	10.7%	Score 142;	DB 2;	Length 227;
Best Local Similarity	30.8%;	Pred. No. 2.7e-05;		
Matches	56;	Conservative 22;	Mismatches 72;	Indels 32; Gaps 10;
QY	39	GWVTGTGGGSLKHGD--EIVAPSGVQKRIQIOPEDMFVCDINPKDISGSPSKLKKSQ	96	
Db	16	GLVKFTWGNVSEVNRRLGVIVIKDSGYDYDELTPENMVVTDLQKILQG	70	
QY	97	CTPLFNWAY--TMRGAGAVIHTHSCAAVMATLLFFGRE---FKITHQEMIKGIKKTSG--	150	
Db	71	DLPTHVOLYKTTWSEIGSWVHTHSTEAV--GWAQAGRDIPFYGTTTHADYFYGSIPCARSLT	128	
QY	151	-----GYRYDDMLVVPILIENTPEEKGLKORMAHMNEYPDSCAVLYRRHGVYTWGETWE	205	
Db	129	KDEVEVAYEKDTGLV--IVSEFP--EHRGLNP-----VEVP---GIVVRNHGPFWTGKNPE	176	
QY	206	KA	207	
Db	177	NA	178	

RESULT 13
AI0977
probable sugar isomerase (EC 5.1.---) [imported] - Salmonella enterica subsp. enterica s

C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: A10977
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulé, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: A10977
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07949.1; PID:gl6504938; GSPDB:GN00176
C:Genetics:
A:Gene: STY4119
C:Superfamily: L-ribulose-phosphate 4-epimerase
C:Keywords: isomerase

	Query Match	10.7%	Score 141;	DB 2;	Length 231;
	Best Local Similarity	30.0%;	Pred. No. 3.4e-05;		
	Matches 65;	Conservative 26;	Mismatches 84;	Indels 42;	Gaps 14
Qy	39	GWVTGTCGGISLKHGDE----	IYTAPSGGVOKERIQEDMFVCDI-NEKDISGPPSPSKLK	93	
Db	20	GLVFTWGNVSAV--DETRKLWVTKPSGVEYEVMTADDMVVVETASGVKVEG----	NKPS	74	
Qy	94	KSQCTPLFM-NAYTMRGAGAVIHTHSCAAVM----	ATLLFPGREPKITHQEMIKGIKCTTS	149	
Db	75	SDTATHLALYRRYPQ--IGGIVHTHSHATIWSQAGLDLPA--WGTTHADIFYGAIPCTR	130		
Qy	150	-----GGYYRYDDMLVPIENTPEBKGLKDRMAHAMNENYPDSCAVLVRHRYGVYVWG-	201		
Db	131	LMTVEEINGEYEQ--TGEVLIKTPEERGLDPA-----QIP----	AVLVHSHGPFPAWGK	178	
Qy	202	---ETWEKAKTMCEC-YDYLFEDIAVSMKKVGLDPSQL	234		
Db	179	NAADAVHNAVVLBECAYMGLFSRQLAPQLPDMQPELL	215		

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RESULT 14
AC3533
1-fuculose phosphate aldolase (EC 4.1.2.17) [imported] - Brucella melitensis (strain 16-
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3533
R:DelVecchio, V.; Kapatal, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3533
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <KUR>
A:Cross-references: UNIPROT:O8YD17; GB:AE008918; PIDN:AAL53430.1; PID:G17984327; GSPDB:C
A:Experimental source: strain 16M

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	Query Match	10.6%	Score 140.5	DB 2	Length 244	
	Best Local Similarity	23.8%	Pred. No. 4e-05			
	Matches 49	Conservative	31	Mismatches 67	Indels 59	Gaps 9
Qy	25	RYLPELCKOFYHLGWVTGGGICSLKHGDEIYIAPSGVKERIQPEDMFVCDINERDIS	84			
Db	37	RQSIDAMRSFEKGFHSGSGNISVREGHIWVTPTGA-TSTWDPDQDMSLVLSGEHLA	95			
Qy	85	GPSPSKKLKSGSOCTPLFMNAYTWRG---AGAVIHTHSKAAVWATLL-----	128			

Search completed: February 1, 2005, 14:30:13
Job time : 42 secs